

**Amendments to the Specification:**

Please replace paragraph [0177] on page 19 of the application as filed, with the following amended paragraph:

**[0177]** The analysis was followed up for the antibody targeted against Hda1, for which it was determined the antibody was raised against a 21 amino acid peptide with the sequence TDGLNNIIIEERFEEATDFILD (SEQ ID NO:22). Comparison of this sequence with the sequence cross comparison of the 7 reactive proteins shows that the region of highest similarity (see Figure 3C) is entirely contained within the 21 amino acid sequence of the peptide (Figure 3D). To confirm this peptide as a common epitope on the proteins that cross-react with the anti-Hda1 antibody, arrays were probed with the antibody in the presence of an excess amount of the immunizing peptide; a peptide of similar length but different sequence was used as a control. As shown in Figure 2C, the Hda1 blocking peptide inhibits the interaction of anti-Hda1 with its cognate antigen Ynl021W-Hda1 as well to each of the seven cross-reacting proteins. No inhibition of anti-Hda1 binding to these proteins was observed with the control peptide.

Please replace paragraph [0191] on page 21 of the application as filed, with the following amended paragraph:

**[0191] Amino Acid Composition of Hda1 blocking peptide.** Anti-Hda1 blocking peptide was purchased from Santa Cruz Biotechnologies, Inc (Santa Cruz, CA; 0.2ug/ul in 1XPBS). Peptide was analyzed for amino acid composition using a Beckman 7300 amino acid analyzer at the HHMI Biopolymer Keck Foundation Bioresearch Laboratory at Yale University. Comparison of the amino acid composition with the linear sequence of Hda1 was used to determine the peptide sequence: TDGLNNIIIEERFEEATDFILD (SEQ ID NO:22).

Please replace paragraph [0192] on page 21 of the application as filed, with the following amended paragraph:

[0192] All antibodies were purchased from commercial vendors (See experimental protocols). ~~For each antibody, the amount of cognate antigen present on the array by [PUT DESCRIPTION OF HOW GST WAS USED TO CALCULATE AMOUNT OF PROTEIN IN METHODS AND REFER TO IT HERE].~~ The antibody concentration used to probe the protein arrays was determined by titrating each antibody for maximal reactivity with its cognate antigen. The number of proteins having a signal to background ratio greater than or equal to 2.0 is reported.

Please replace paragraph [0195] on page 22 of the application as filed, with the following amended paragraph:

[0195] In order to assess the utility of sequence analysis in predicting cross reactivity, all yeast proteins were searched for either the 8 amino acid epitope core sequence NNIEERF (SEQ ID NO:1) or the 20/21 amino acid immunogenic peptide sequence TDGLNNIEERFEEATDFILD (SEQ ID NO:22). The top matches are presented in Table 4. In addition to the observed cross-reactive proteins, a large number of proteins are identified with similarly high sequence conservation which show no empirical evidence of cross reactivity. Thus, although sequence analysis is useful in explaining the observed cross-reactivity, it is clearly insufficient to predict it.

**Table 2.** Sequence alignments for the 3 regions of highest homology based on a comprehensive 8 amino acid window sequence comparison. Sequence alignment is shown for 12 amino acids – the 8 amino acid core (bold in all, underlined for reference sequence YNL021W) and 2 amino acids on both N' and C'. Identities are in red.

<u>Sequence</u> <u>core)</u>	<u>Protein</u>	<u>Identity (in 8 aa</u>
Region 1		
EE <b><u>ENSLSTTSKS</u></b> ( <u>SEQ ID NO:2</u> )	YNL021W	
ES <b><u>EESSTNSVI</u></b> ( <u>SEQ ID NO:3</u> )	YDR469W	.625
EQ <b><u>ADSSSLTSFS</u></b> ( <u>SEQ ID NO:4</u> )	YLR332W	.5
VM <b><u>ENLLTTAGVS</u></b> ( <u>SEQ ID NO:5</u> )	YMR110C	.5
TD <b><u>EGSYSTSIKS</u></b> ( <u>SEQ ID NO:6</u> )	YDL204W	.5

Region 2

FN <b>EPINDSII</b> SK (SEQ ID NO:7)	YNL021W	
GG <b>EPINSSVA</b> SN (SEQ ID NO:8)	YLR332W	.625
KN <b>EPYIDKII</b> SK (SEQ ID NO:9)	YDL204W	.625
FN <b>ETINKIIE</b> SK (SEQ ID NO:10)	YMR110C	.5
MN <b>YLIEQSNILK</b> (SEQ ID NO:11)	YDR469W	.375

### Region 3

GL <b>NNIIIEERFEE</b> (SEQ ID NO:12)	YNL021W	
AS <b>NDIIEEKFYD</b> (SEQ ID NO:13)	YLR332W	.75
T <b>INKIIEEH</b> DTP (SEQ ID NO:14)	YMR110C	.625
NQ <b>NVKIEESSE</b> P (SEQ ID NO:15)	YDR469W	.5
NL <b>FNNEHENFDE</b> NL <b>FNNRHENFDE</b> (SEQ ID NO:16)	YDL204W	.375

Please replace paragraph [0196] on page 22 of the application as filed, with the following amended paragraph:

[0196]

**Table 3.** Sequence alignment of the immunogenic peptide region with best matches from each of the 4 ‘cross-reactive’ proteins. The 8 amino acid core from region 3 (Figure 1) is in bold for all sequences, and underlined in the reference sequence

<u>Sequence</u>	<u>Protein</u>
TDGL <b><u>NNIIIEERFEE</u></b> ATDFILD (SEQ ID NO:17)	YNL021W
SVAS <b><u>NDIIEEKFY</u></b> DEQGNELS (SEQ ID NO:18)	YLR332W
KDFH <b><u>RNKIESVLNET</u></b> TKLMND (SEQ ID NO:19)	YMR110C
FHKN <b><u>YNKVVEKTE</u></b> PYIDKIIP (SEQ ID NO:20)	YDL204W
SSST <b><u>NSVIEESSE</u></b> PKISKLEN (SEQ ID NO:21)	YDR469W

Please replace paragraph [0197] on pages 22 and 23 of the application as filed, with the following amended paragraph:

[0197]

**Table 4.**

<b><u>Sequence</u></b>	<b><u>Protein</u></b>	<b><u>Identity</u></b>
TDGLNNIIIEERFEEATDFILD ( <u>SEQ ID NO:22</u> )	YNL021W	1.000
TNGRNIIIEEIEASRTSFTLY ( <u>SEQ ID NO:23</u> )	YDR291W	0.476
TDYLNKNIIVENSGTSGDEDVD ( <u>SEQ ID NO:24</u> )	YIL075C	0.429
RDYLSYIEERLQEEHLDINN ( <u>SEQ ID NO:25</u> )	YKL201C	0.429
KTDLVNFIEERFKTFCDEELE ( <u>SEQ ID NO:26</u> )	YKR054C	0.429
TVLENKKIEEGKETAVDREED ( <u>SEQ ID NO:27</u> )	YKL188C	0.429
IEGLNIISSGTFESLQDFVLQ ( <u>SEQ ID NO:28</u> )	YNL193W	0.429
TDASNGYDEELPEEEQEFSD ( <u>SEQ ID NO:29</u> )	YNL124W	0.429
SYLNCIIIEENFKEMTRKLQR ( <u>SEQ ID NO:30</u> )	YNL126W	0.429
GQFLENFLELNLNEVTDLIRD ( <u>SEQ ID NO:31</u> )	YDR481C	0.381
TLSAGNACPGWDEDANDDILD ( <u>SEQ ID NO:32</u> )	YBR092C	0.381
TDIFKNCLNQFEITNLKILF ( <u>SEQ ID NO:33</u> )	YKL057C	0.381
DDDDDDDEDEEEEEVTDQLED ( <u>SEQ ID NO:34</u> )	YFR033C	0.381
VDGKGNETEEDDIKFIKGILD ( <u>SEQ ID NO:35</u> )	YJL168C	0.381
DDGLPNGITLIGKKFTDYALL ( <u>SEQ ID NO:36</u> )	YBR208C	0.381
TISLIHEIEKIFEEDIHFEQN ( <u>SEQ ID NO:37</u> )	YHR184W	0.381
FQGGLDIIKESLEEDPDFLQH ( <u>SEQ ID NO:38</u> )	YDR098C	0.381
TDYLFDYREVLESGLDIILD ( <u>SEQ ID NO:39</u> )	YLR443W	0.381
QFLLSKIIIEARISGAFFEIWD ( <u>SEQ ID NO:40</u> )	YDL231C	0.381
TEFYNNYSMQVREDERDYILD ( <u>SEQ ID</u>	YDL040	0.381

**Sequence**

**Protein**

**Identity**

NO: 41)